RAW SEQUENCE LISTING PATENT APPLICATION US/08/726,211

DATE: 11/09/96 TIME: 16:23:16

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This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING TERED 1 2 3 General Information: (1) (i) APPLICANT: Tormo, Mar 5 Tari, Ana M. 6 7 Lopez-Berestein, Gabriel 8 (ii) TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY 9 LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES 10 11 12 (iii) NUMBER OF SEQUENCES: 7 13 (iv) CORRESPONDENCE ADDRESS: 14 (A) ADDRESSEE: Arnold, White & Durkee 15 (B) STREET: P.O. Box 4433 16 17 (C) CITY: Houston (D) STATE: Texas 18 (E) COUNTRY: United States of America 19 20 (F) ZIP: 77210 21 22 (V) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk 23 (B) COMPUTER: IBM PC compatible 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 26 27 28 (vi) CURRENT APPLICATION DATA: 29 (A) APPLICATION NUMBER: US Unknown (B) FILING DATE: Concurrently Herewith 31 (C) CLASSIFICATION: Unknown 32 (viii) ATTORNEY/AGENT INFORMATION: 33 34 (A) NAME: Wilson, Mark B. (B) REGISTRATION NUMBER: 37,259 35 (C) REFERENCE/DOCKET NUMBER: UTXC:504 36 37 (ix) TELECOMMUNICATION INFORMATION: 38 (A) TELEPHONE: (512) 418-3000 39 (B) TELEFAX: (512) 474-7577 40 41 42 43 (2) INFORMATION FOR SEQ ID NO:1: 44 (i) SEQUENCE CHARACTERISTICS: 45 46 (A) LENGTH: 18 base pairs

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	INPUT SET	r: S13733.raw
47	(B) TYPE: nucleic acid	
48	(C) STRANDEDNESS: single	
49	(D) TOPOLOGY: linear	
50		
51	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
52		
53	CAGCGTGCGC CATCCTTC	18
54		
55		
56	(2) INFORMATION FOR SEQ ID NO:2:	
57	(2) INFORMATION FOR SEQ 15 NO.2.	
	(i) CHOURNER CHARACTERISE.	
58	(i) SEQUENCE CHARACTERISTICS:	
59	(A) LENGTH: 20 base pairs	
60	(B) TYPE: nucleic acid	
61	(C) STRANDEDNESS: single	
62	(D) TOPOLOGY: linear	
63		ų.
64		
65	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
66		
67	ACGGTCCGCC ACTCCTTCCC	20
68		
69		
70	(2) INFORMATION FOR SEQ ID NO:3:	
71		
72	(i) SEQUENCE CHARACTERISTICS:	
73	(A) LENGTH: 16 base pairs	
74	(B) TYPE: nucleic acid	
75	(C) STRANDEDNESS: single	
76	(D) TOPOLOGY: linear	
77	(2) 101020011 1111001	
78	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
79	(AI) BEGGENEE BESCHILLIEN. BEG IS NO. 3.	
80	CTGAAGGGCT TCTTCC	16
81	CIGARGUET TETTEE	10
82		
83	(2) INFORMATION FOR GEO ID NO.4.	
	(2) INFORMATION FOR SEQ ID NO:4:	
84	(i) GROUPING GUIDI GERDEGE	
85	(i) SEQUENCE CHARACTERISTICS:	
86	(A) LENGTH: 5086 base pairs	
87	(B) TYPE: nucleic acid	
88	(C) STRANDEDNESS: single	
89	(D) TOPOLOGY: linear	
90		
91	(ix) FEATURE:	
92	(A) NAME/KEY: CDS	
93	(B) LOCATION: 14592175	
94		
95	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
96	· · · -	
97	GCGCCGCCC CTCCGCGCCG CCTGCCCGCC CGCCCGCC	rcc 60
98		
99	GTGGCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA GGTGCCGGGG CTCCGGGC	CCC 120
	TITTE STORY	

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TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC GAACTGCGCG ACGGGAGGTC CGGGAGGCGA CCGTAGTCGC GCCGCCGCG AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG GGGTGCGCCG GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGGAGAACTT CGTAGCAGTC ATCCTTTTTA GGAAAAGAGG GAAAAAATAA AACCCTCCCC CACCACCTCC TTCTCCCCAC CCCTCGCCGC ACCACACA GCGCGGGCTT CTAGCGCTCG GCACCGGCGG GCCAGGCGCG TCCTGCCTTC ATTTATCCAG CAGCTTTTCG GAAAATGCAT TTGCTGTTCG GAGTTTAATC AGAAGACGAT TCCTGCCTCC GTCCCCGGCT CCTTCATCGT CCCATCTCCC CTGTCTCTCT CCTGGGGAGG CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA ATACCGGACT GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA AACTCGAGCT CTTGAGATCT CCGGTTGGGA TTCCTGCGGA TTGACATTTC TGTGAAGCAG AAGTCTGGGA ATCGATCTGG AAATCCTCCT AATTTTTACT CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA TCAGCTATAA CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG GTTTTACAAA AAGGAAACTT GACAGAGGAT CATGCTGTAC TTAAAAAAATA CAAGTAAGTC TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC CTTTGAGATT TTTTACTTAA AGTGCATTCG AGTAAATTTA ATTTCCAGGC AGCTTAATAC ATTGTTTTTA GCCGTGTTAC TTGTAGTGTG TATGCCCTGC TTTCACTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA CTTATTAGTT TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA TTGGAATAAA AATTTCCTGC GTCTCATGCC AAGAGGGAAA CACCAGAATC AAGTGTTCCG CGTGATTGAA GACACCCCT CGTCCAAGAA TGCAAAGCAC ATCCAATAAA ATAGCTGGAT TATAACTCCT CTTCTTTCTC TGGGGGCCGT GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT GCTTTTCCTC TGGGAAGG ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn CGG GAG ATA GTG ATG AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly

RAW SEQUENCE LISTING PATENT APPLICATION US/08/726,211

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TAC GAG TGG GAT GCG GGG GAT GCG GGC GCC CCG GGG GCC GCC 1587															IN	<i>IPUT</i>	SET:	S13733.raw
154 Tyr Clu Tyr Sap Ala Cly Ala Cly Ala Ala Pro Pro Cly Ala Ala Ala Pro Pro Cly Ala Ala Ala Ala Pro Pro Cly Ala Ala Ala Pro Pro Cly Ala Ala Ala Pro Pro Ala Pro Cly Tie Pro Ser Ser Cln Pro Cly His Thr Pro His Pro Ala Pro Ala Pro Cly Tie Pro Ala Ala Ala Pro Pro Ala Ala Ala Ala Pro Cly Ala Ala Ala Ala Ala Pro Pro Ala Ala Ala Ala Ala Pro Pro Ala Ala	153	TAC	GAG	TGG	GAT	GCG	GGA	GAT	GTG	GGC	GCC	GCG	CCC	CCG				
155																		
156		-1-					1		_	,					1			
157														- •				
158		CCC	GCA	CCG	GGC	ልጥሮ	ጥጥር	TCC	TCC	CAG	CCC	aga	CAC	ACG	CCC	СУТ	CCA	1635
159																		1033
161		FIO		FIO	СТУ	116	FILE		261	GIN	FIO	GLY		1111	PIO	IIIS	FIG	
161			43					30					33					
162		000	003	maa	000	ana	000	ama	000	3.00	3.00	maa	000	C/m/C	ana	200	000	1602
163																		1003
164			АТА	ser	Arg	ASP		vaı	Ala	Arg	THE		PIO	Leu	GIN	THE		
165		60					65					70					75	
166		aam	000	aaa	000	000	000	999	222	aam	222	ama	100	000	ama	aa .	aam	1721
168																		1/31
168		Ата	АТа	Pro	GTA		АТа	АТа	GTA	Pro		Leu	Ser	Pro	vaı		Pro	
179						80					85					90		
171																		
172																		1779
172		Val	Val	His		Ala	Leu	Arg	GIn		GTÀ	Asp	Asp	Phe		Arg	Arg	
TAC					95					100					105			
Tyr																		
175 TTC ACC GCG GGA CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG ACG TTC ACG ACG ACG ACG GTG GTG GAG GAG GTC TTC AGG ACG ACG																		1827
176		Tyr	Arg	_	Asp	Phe	Ala	Glu		Ser	Ser	Gln	Leu		Leu	Thr	Pro	
TTC				110					115					120				
178																		
179	177																	1875
181 GAC GGG GTG AAC TGG GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG 1923 181 ASP Gly Val ASN Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly 155 155 184 140 145 145 150 150 155 184 185 GTC ATG TGT GTG GAG AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC ACC 186 160 160 ASN ARG GLU MET SER PRO LEU Val ASN ARG 170 165 170 188 AAC ATC GCC CTG TGG ATG ATG ACT GAG TAC CTG AAC CTG CAC ACC 170 165 170 170 188 ASN Ile Ala Leu Trp Met Thr Glu Tyr Leu ASN ARG HIS Leu HIS Thr 175 180 ASN ARG HIS Leu HIS Thr 185 199 ASN Ile GAT CAG GAT AAC GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC 2067 2067 194 Trp Ile Gln ASP ASN Gly Gly Trp ASP Ala Phe Val Glu Leu Tyr Gly 195 190 200 196 197 CCC AGC ATG CGG CCT CTG TTT GAT TTC TCC TGG CTG TCT TCT CTG AAG ACT 2115 198 Pro Ser Met Arg Pro Leu Phe ASP Phe Ser Trp Leu Ser Leu Lys Thr 215 199 205 210 200 215 200 225 220		Phe	Thr	Ala	Arg	Gly	Arg	Phe	Ala	Thr	Val	Val	Glu	Glu	Leu	Phe	Arg	
181 GAC GGG GTG AAC TGG GGG AGG ATT GTG GCC TTC TTT GAG TTC GGG GGG GGG 1923 182 ASP GIV Val ASN TTP GIV Arg Ile Val Ala Phe Glu Phe Ala Phe Glu Phe Ala Phe	179		125					130					135					
182	180																	
183 140 145 150 155 184 185 GTC ATG TGT GTG GAG AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC 1971 186 Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp 160 165 170 187 160 165 170 188 AAC ATC GCC CTG TGG ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC 2019 190 Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr 175 180 185 192 193 TGG ATC CAG GAT AAC GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC 2067 2067 194 Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly 195 200 196 190 195 200 197 CCC AGC ATG CGG CCT CTG TTT GAT TTC TCC TGG CTG TCT CTG AAG ACT 2115 198 Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr 210 205 200 201 215 202 205 210 201 225 230	181																	1923
184		Asp	Gly	Val	Asn	Trp	Gly	Arg	Ile	Val	Ala	Phe	Phe	Glu	Phe	Gly	Gly	
185	183	140					145					150					155	
186 Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp 187 188 189 AAC ATC GCC CTG TGG ATG ACT GAG TAC CTG AAC CGG CAC ACC 2019 190 Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Thr 191 191 175 Trp Met Thr Glu Tyr Leu Asn Arg His Thr Thr 185	184																	
187 160 165 170 188 189 AAC ATC GCC CTG TGG ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC 2019 190 Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr 191 175 180 185 185 192 193 TGG ATC CAG GAT AAC GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC 2067 2067 194 Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly 200 200 196 197 CCC AGC AGC ATG CGG CCT CTG TTT GAT TTC TCC TGG CTG TCT CTG AAG ACT 2115 198 Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr 215 200 201 215 201 CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT 2163 202 Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr 235 203 220 225 230 235	185	GTC	ATG	TGT	GTG	GAG	AGC	GTC	AAC	CGG	GAG	ATG	TCG	CCC	CTG	GTG	GAC	1971
188 189 AAC ATC GCC CTG TGG ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC 2019 190 Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr 185 191 175 180 185 192 193 TGG ATC CAG GAT AAC GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC 2067 194 Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly 195 200 196 190 195 200 197 CCC AGC ATG CGG CCT CTG TTT GAT TTC TCC TGG CTG TCT CTG AAG ACT 2115 198 Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr 215 200 201 CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT 2163 202 Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr 235 203 220 225 230 235	186	Val	Met	Cys	Val	Glu	Ser	Val	Asn	Arg	Glu	Met	Ser	Pro	Leu	Val	Asp	
189 AAC ATC GCC CTG TGG ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC 2019 190 Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr 191 TGG ATC CAG GAT AAC GGA GGC TGG GAT Leu His Thr 192 TGG ATC CAG GAT AAC GGA GGC TGG GAT CTG TAC GGC 2067 194 Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly 195 Tgg Tgg TTG TTG <td< td=""><td>187</td><td></td><td></td><td></td><td></td><td>160</td><td></td><td></td><td></td><td></td><td>165</td><td></td><td></td><td></td><td></td><td>170</td><td></td><td></td></td<>	187					160					165					170		
190	188																	
191	189	AAC	ATC	GCC	CTG	TGG	ATG	ACT	GAG	TAC	CTG	AAC	CGG	CAC	CTG	CAC	ACC	2019
192 193	190	Asn	Ile	Ala	Leu	Trp	Met	Thr	Glu	Tyr	Leu	Asn	Arg	His	Leu	His	Thr	
193 TGG ATC CAG GAT AAC GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC 194 Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly 195 190 195 200 196 197 CCC AGC ATG CGG CCT CTG TTT GAT TTC TCC TGG CTG TCT CTG AAG ACT 198 Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr 199 205 210 215 200 201 CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT 202 Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr 203 220 225 230 235 204	191				175					180					185			
194 Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly 195	192																	
195	193	TGG	ATC	CAG	GAT	AAC	GGA	GGC	TGG	GAT	GCC	TTT	GTG	GAA	CTG	TAC	GGC	2067
196 197	194	Trp	Ile	Gln	Asp	Asn	Gly	Gly	Trp	Asp	Ala	Phe	Val	Glu	Leu	Tyr	Gly	
197	195	_		190	_				195					200				
198 Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Leu Leu Leu Leu Ser Leu Leu Leu Leu Ser Leu S	196																	
199 205 210 215 200 201 CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT 2163 202 Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr 203 220 225 230 235 204	197	CCC	AGC	ATG	CGG	CCT	CTG	TTT	GAT	TTC	TCC	TGG	CTG	TCT	CTG	AAG	ACT	2115
199 205 210 215 200 201 CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT 2163 202 Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr 203 220 225 230 235 204	198																	
200 201 CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT 202 Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr 203 220 225 230 235 204	199				_				-			-				_		
201 CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT 202 Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr 203 220 225 230 235 204																		
202 Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr 203 220 225 230 235 204		CTG	CTC	AGT	TTG	GCC	CTG	GTG	GGA	GCT	TGC	ATC	ACC	CTG	GGT	GCC	TAT	2163
203 220 225 230 235 204																		
204											2 -				4		_	
	205	CTG	AGC	CAC	AAG	TGA	AGTC!	AAC A	ATGC	CTGCC	CC CI	AAAC	AAAT	A TGC	LAAA	AGGT		2215

RAW SEQUENCE LISTING PATENT APPLICATION US/08/726,211

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						MEOL SEL SIS/S	J.IUW
206	Leu Ser His	s Lys					
207							
208	manamanaa	10m10111m	AMAMOO AMMO	ma sama smam	ACCIATICA A AC	AAAGCTGCAG	2275
209	TCACTAAAGC	AGTAGAAATA	ATATGCATTG	TCAGTGATGT	ACCATGAAAC	AAAGCTGCAG	2213
210	CCMCMMM > > C	*********	3.G3.G3.M3.M3.3	A CAMCACACA	GAGAGAGA	GAGAGAGA	2225
211	GCTGTTTAAG	AAAAAATAAC	ACACATATAA	ACATCACACA	CACAGACAGA	CACACACA	2335
212	G1G11G11MM	11010mamma	1000111100	maaa amaa aa	mamma amaa	GAAAGGGAAA	2395
213	CACAACAATT	AACAGTCTTC	AGGCAAAACG	TCGAATCAGC	TATTTACTGC	CAAAGGGAAA	2395
214	m.ma.mmm.m		,mm,,,,,,,,,	3 3 G 3 MMM 3 MM	mammaa.ca.c	A CITICO CA A TICA	2455
215	TATCATTTAT	TTTTTACATT	ATTAAGAAAA	AAGATTTATT	TATTTAAGAC	AGTCCCATCA	2455
216	amaaama	mmmaa	GG1 GG1 GM11	mmaaaa a .	aaaammaama	тааатаа каа	2515
217	AAACTCCGTC	TTTGGAAATC	CGACCACTAA	TTGCCAAACA	CCGCTTCGTG	TGGCTCCACC	2515
218		amaaamam	101m101mm	aammmaa s ma	mmammaaaaa	a.ma.aa.ma	0535
219	TGGATGTTCT	GTGCCTGTAA	ACATAGATTC	GCTTTCCATG	TIGTIGGCCG	GATCACCATC	2575
220				, ma, mmaaaa		mamaaamaam	0605
221	TGAAGAGCAG	ACGGATGGAA	AAAGGACCTG	ATCATTGGGG	AAGCTGGCTT	TCTGGCTGCT	2635
222		a. a aamam	mas mmas amm	001	0000m00000	GGMG 3 M 3 MM 3	2605
223	GGAGGCTGGG	GAGAAGGTGT	TCATTCACTT	GCATTTCTTT	GCCCTGGGGG	CGTGATATTA	2695
224			22222112ma	a.maaamaaa	maaaamaaaa	1101010mam	0755
225	ACAGAGGGAG	GGTTCCCGTG	GGGGGAAGTC	CATGCCTCCC	TGGCCTGAAG	AAGAGACTCT	2755
226				maaa.aa	1010000000	1 CMMC 1 C 1 MC	2015
227	TTGCATATGA	CTCACATGAT	GCATACCTGG	TGGGAGGAAA	AGAGTTGGGA	ACTTCAGATG	2815
228	a	aa.ama.a.m	mmaa		1maaa11111	magaamma a a	2075
229	GACCTAGTAC	CCACTGAGAT	TTCCACGCCG	AAGGACAGCG	ATGGGAAAAA	TGCCCTTAAA	2875
230				mmamaaaa.a		m	2025
231	TCATAGGAAA	GTATTTTTT	AAGCTACCAA	TTGTGCCGAG	AAAAGCATTT	TAGCAATTTA	2935
232				mmamamamamam		maa.m.aaa.	2005
233	TACAATATCA	TCCAGTACCT	TAAACCCTGA	TTGTGTATAT	TCATATATTT	TGGATACGCA	2995
234	GGGGGGA 1 GE	GGGN NEW GEO	аатататата	10m1101110	3.03.3 M.C.C.M.C.M.	aaa aammaaa	3055
235	CCCCCCAACT	CCCAATACTG	GCTCTGTCTG	AGTAAGAAAC	AGAATCCTCT	GGAACTTGAG	3033
236	a ama a.	mmmaaama sa	mmaga h maha	GA A GGGTTA GA	CHILL COOK OF	GGAMGAGGGG	2115
237	GAAGTGAACA	TTTCGGTGAC	TTCCGATCAG	GAAGGCTAGA	GTTACCCAGA	GCATCAGGCC	3115
238	00010110m0	CCMCCMMMM 3	0010100011	amaaaaa aa a	aam x aamama	maaa kaamma	3175
239	GCCACAAGTG	CCTGCTTTTA	GGAGACCGAA	GICCGCAGAA	CCIACCIGIG	TCCCAGCTTG	31/3
240	а в а а а а а а а а а а а а а а а а а а	GGTTGG 3 3 GTTG	***************************************	ma kamaaaam	GGMGG A GGG A	maamaa aaaa	3235
241	GAGGCCTGGT	CCTGGAACTG	AGCCGGGCCC	TCACTGGCCT	CCTCCAGGGA	TGATCAACAG	3233
242	COMP CHICAGO	mamaaaa a ama	татаа хаат	CAMOCAMOCA	CCTC A C A A TITO	CC A CTTCTTC A A	3295
243	GGTAGTGTGG	TCTCCGAATG	TUTGGAAGUT	GATGGATGGA	GCTCAGAATT	CCACTGTCAA	3293
244	aa.a.a.a	ma da deceme	тааатааааа	TGTCACCCTG	aaaaaamaa k	COM A COCCO	3355
245	GAAAGAGCAG	TAGAGGGGTG	TGGCTGGGCC	TGTCACCCTG	GGGCCCTCCA	GGTAGGCCCG	3333
246	mmmma a como	GA GGAMA GGA	000200200	mmamma a a a a	3 M C M 3 M C 3 C M	CITA CA CCCA A	3415
247	TTTTCACGTG	GAGCATAGGA	GCCACGACCC	TTCTTAAGAC	AIGIAICACI	GTAGAGGGAA	3413
248	0011010100	aaamaaaaaa	maamamaaaa	ACCACAMOOM	C B B C C C TT C C C	* * CCTC * CC *	2475
249	GGAACAGAGG	CCCTGGGCCT	ICCIATCAGA	AGGACATGGT	GAAGGCTGGG	AACGTGAGGA	3475
250	GA GGGA A MGG	aaraaaaaa	mmmmaaamam	ACCACAMOCC	A COMPOCOPO	TOTO COMMO	3535
251	GAGGCAATGG	CCACGGCCCA	TTTGGCTGT	AGCACATGGC	ACGITGGCTG	TGTGGCCTTG	3333
252	OCC & COMOTO	3.CMMM3.3.3.CC	3 3 CCCCMMM 2 2	A M C A C M C C	A C A C C C C C C C C C C C C C C C C C	АААТССТААА	3595
253	GCCACCTGTG	AGTITAAAGC	AAGGCTTTAA	ATGACTTTGG	AGAGGGTCAC	AAATCCTAAA	3373
254	ACA ACCAMMC	A A CITICA A COMO	maxmaaxmm:	AMMO A COCOM		መመል (18 መረመል 8	3655
255 256	AGAAGCATTG	AAGTGAGGTG	ICAIGGATTA	ATTGACCCCT	GICIATGGAA	TTACATGTAA	3033
256 257	3 3 C 3 MM 3 M C M	mama kamam k			CMC V C V V V V V	AAAAGTTCCA	3715
257	AACATTATCT	TGTCACTGTA	GITTGGTTTT	ATTIGAAAAC	CIGACAAAAA	AAAAGITUUA	3/13
258							